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Estimation of genetic parameters and trends for morphometric traits in Brazilian Mangalarga Marchador horses

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ABSTRACT - The objective of this work was to estimate genetic parameters and evaluate genetic trends over 26 years for morphometric traits in Mangalarga Marchador horses. Twelve morphometric traits were evaluated (withers and croup heights; length of head, body, shoulder, croup, neck, back, and loins; width of head and croup, and cannon bone and thorax perimeters). These traits were evaluated in 38,341 animals born between 1987 and 2012 and with a relationship matrix of 77,719 animals. Gibbs sampler was used to obtain samples of the posterior distributions of genetic parameters under animal models. Genetic trends were estimated by regression of estimated breeding values in function of birth year. The heritabilities of all traits were moderate to high and ranged from 0.27 to 0.48. However, the additive genetic coefficients of variation were low, ranging from 1.23 to 3.82%. The genetic trends of all the studied traits were significant, but of low magnitude. Negative genetic trend was observed for body length, while positive genetic trends were estimated for the other 11 traits. Although additive genetic differences accounted for a significant part of the phenotypic differences, genetic gains in the population were limited by low phenotypic variability. Therefore, it is necessary to develop data collection strategies to increase phenotypic and genetic variability in the population, such as the inclusion of animals that do not meet breed standard, but which have parents registered in the breeders' association, in the database.

Keywords: equine, genetic gain, heritability, phenotypic selection

1. Introduction

Brazil has the fourth largest horse herd in the world, with approximately 5.5 million animals (Gilbert et al., 2018). Mangalarga Marchador is the most representative breed, with approximately 600,000 live animals (Lima and Cintra, 2016). Additional information about population structure and genetic diversity of this breed might be found in Baena et al. (2020). The equideoculture sector generates over 16 billion reais a year in Brazil, generating direct and indirect jobs for about three million people (Lima and Cintra, 2016). Horses have large participation in the agribusiness in Brazil, being their main contribution related to the daily management in the rural properties, and their traits related to the locomotion are important – being the gait the more commonly studied. The evaluation of morphometric traits makes it possible to infer at the potential of an animal for gait, based on the assumption that some morphometric traits are genetically correlated with traits related to gait, as walk and trot stride length and impulsion (Rustin et al., 2009; Vicente et al., 2014). Besides the association with gait, the economic value of horses is commonly associated to how close to the breed standard conformation, determined by the association of breeders, the horse is. For all the reasons cited above, the morphometric patterns usually direct the sense of selection practiced in equine breeds (Meira et al., 2013; Sousa et al., 2018).

The direct evaluation of gait is, in general, onerous, time consuming, and requires many resources for its accomplishment when compared with the evaluation of morphometric traits. Therefore, evaluating gait by means of morphometric measures that are moderately or strongly associated with it allows better targeting of resources for animals that actually possess desirable abilities to function (Sánchez-Guerrero et al., 2017). Genetic correlations of the order of 0.2-0.4 were found between conformation and competition results for Swedish Warmblood riding horses (Wallin et al., 2003). The genetic correlations between the linear traits and dressage traits ranged between 0 (walk and head width) and 0.46 (canter angle of shoulder) for Pura Raza Español horses (Sánchez-Guerrero et al., 2017). For Thoroughbred horses, Paksoy and Ünal (2019) estimated correlations varying from 0.12 between height at withers and front chest width to 0.68 between height at withers and height at croup, but the authors concluded that the examined morphometric measurements are not significant to predict race performance for this breed.

It is important to highlight that these breeds have a different type of gait in comparison with Mangalarga Marchador, which has the marcha with threefold support as type of gait (ABCCMM, 2020). During the walk, the Mangalarga Marchador feet are in constant contact with the ground, which provide greater comfort to the rider. This difference can reflect in changes in the behavior of the genetic parameters for both gait and morphometry when compared with other breeds, and until now, no genetic parameters have been estimated for morphometric traits of Mangalarga Marchador horses.

The use of estimated breeding values (EBV) for linear traits in equines can make selection for conformation and gait more effective (Rustin et al., 2009). Considering the genetic parameters and EBV for morphometric traits allows to select the animals based on its genetic merit and design breeding programs for equine breeds (Sánchez-Guerrero et al., 2017). So far, there is no official breeding program for Margalarga Marchador breed, neither there are well defined selection criteria to be considered in the breeding program. The results of the present study can guide the inclusion of morphometric traits in breeding programs of the breed. For Belgian Warmblood horses, the use of conformation traits as selection criteria in the breeding program is already a common practice, due to their association with the functional ability of the horses (Rustin et al., 2009).

Considering the association between gait and morphometry and the importance of breed pattern for defining the economic value of Mangalarga Marchador horses, it is reasonable to genetically evaluate potential traits to be selected. Evaluating the trend of EBV over the years provides an overview of how the morphometric traits of Mangalarga Marchador horses responded to genetic selection. Furthermore, the genetic parameters can help breeders to verify the traits that are more prone to change throughout selection. This study was conducted to assist breeders in direction of horse breeding. Therefore, the objective of this work was to estimate genetic parameters and evaluate the genetic trends of morphometric traits of Mangalarga Marchador horses over 26 years of evaluation.

2. Material and Methods

The data file used in the present study was provided by the Serviço de Registro Genealógico of the Associação Brasileira dos Criadores do Cavalo Mangalarga Marchador (ABCCMM). The data set comprised of 38,341 records of horses born between 1987 and 2012 and belonging to 1,169 farms throughout the Brazilian territory.

Twelve linear traits measured by certified technicians trained by ABCCMM were evaluated in uncastrated females or males, born and raised until the date of definitive registration in the same farm, registered between three and five years, born between 1987 and 2012, and belonging to farms with 10 or more animals. All evaluated animals: had the definitive register in the ABCCMM, were from three to five years old, had known sire and dam, and had valid records for all 12 linear measures. The traits were (Table 1): withers height (WH); croup height (CH); head length (HL); body length (BL); shoulder length (SL); croup length (CL); neck length (NL); back and loin length (BLL); head width (HW); croup width (CW); cannon bone perimeter (CBP); and thorax perimeter (TP), as described by Cabral et al. (2004) and Sousa et al. (2018). The summary statistics for the data file considered are presented in Table 2.

The relationship matrix was composed of 77,719 animals, with generation coefficient varying from 0 to 2.63. The generation coefficient of each animal was determined from the oldest to the youngest animals, in function of the generation of the parents as $(GC_{P1} + GC_{P2})/2 + 1$, in which GC is the generation coefficient of each parent (P1 and P2). Animals of the base population had GC = 0. The pedigree file had

Table 1 - Descriptions of morphometric traits examined in the research

Traits	Abbreviation	Definition
Withers height	WH	Highest point of the interscapular region, located in the space defined by the spinous process of T5 and T6, until the ground
Croup height	CH	Highest point of the croup, on the sacral tuberosity, to the ground
Head length	HL	Distance between the nuchal crest and the medial or central portion of the lower incisor arch
Body length	BL	Distance between the cranial portions of the greater tubercle of the humerus and caudal of the ischial tuberosity
Shoulder length	SL	Distance between the dorsal edge of the scapular cartilage and the distal angle of the scapula
Croup length	CL	Distance between the cranial portions of the iliac tuberosity and caudal ischial tuberosity
Neck length	NL	Distance between the cranial portion of the dorsal arch of the atlas and the middle third of the cranial edge of the scapula
Back and loin length	BLL	Distance between the ends of the spinous processes of T8 and T9 and the cranial portion of the sacral tuberosity
Head width	HW	Distance between the free portion of the right supraorbital border and the left border
Croup width	CW	Distance between the lateral portions of the iliac tuberosities
Cannon bone perimeter	CBP	Circumference of the metacarpal bones II, III, and IV
Thorax perimeter	TP	Circumference between the spinous processes T8 and T9, passing through the intercostal space of the 8th and 9th ribs, until the articulation of the last rib with the xiphoid process

Table 2 - Summary statistics for morphometric traits of Mangalarga Marchador horses

Trait[1]	n	Mean (cm)	SD (cm)	Min (cm)	Max (cm)	CV (%)
WH	38,431	146.71	3.56	140	171	2.43
CH	38,431	145.67	3.38	135	157	2.32
HL	38,431	56.41	2.02	42	87	3.58
BL	38,431	149.13	4.13	133	176	2.77
SL	38,431	51.29	2.39	40	68	4.66
CL	38,431	50.58	2.69	36	63	5.32
NL	38,431	60.81	2.97	40	80	4.88
BLL	38,431	48.58	3.64	35	68	7.49
HW	38,431	19.88	1.21	17	32	6.07
CW	38,431	49.51	2.11	39	62	4.27
CBP	38,431	17.91	0.84	15	26	4.70
TP	38,431	171.11	5.76	143	197	3.36

n - number of records; SD - standard deviation; Min - minimum; Max - maximum; CV - coefficient of variation.

[1] Abbreviations and definitions of traits, see Table 1.

6,956 stallions with 5.52 foals on average (minimum = 1, maximum = 326) and 24,076 mares with 1.60 foals on average (minimum = 1, maximum = 27).

Sixty-six two-trait analyzes using animal models were carried out to estimate variance components and genetic parameters. We used a Bayesian approach to obtain samples of the posterior distributions of parameters. The systematic effects of age at the evaluation, sex (two levels), farm (1,169 levels), year (26 levels) and month (12 levels) of registration, and random genetic additive and residual effects were considered. The two-trait model can be represented in the following matrix formula:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & \phi \\ \phi & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & \phi \\ \phi & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \tag{1}$$

in which y_h = vector of observations of the morphometric traits (h = WH, CH, HL, BL, SL, CL, NL, BLL, HW, CW, CBP, TP), X_h = matrix of incidence of systematic effects of trait h, b_h = solution vector for the systematic effects, Z_h = matrix of incidence of random of trait h, a_h = vector with the solutions for genetic additive effects, and e_h = the error associated with each observation.

The following assumptions were considered for the effects included in the two-trait model:

$$\begin{bmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{bmatrix} \sim MVN \left\{ \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \begin{bmatrix} A\sigma^2_{a_1} & A\sigma_{a_1,a_2} & 0 & 0 \\ & A\sigma^2_{a_2} & 0 & 0 \\ & & I\sigma^2_{e_1} & I\sigma_{e_1,e_2} \\ sym & & & I\sigma^2_{e_2} \end{bmatrix} \right\} \tag{2}$$

in which MVN = multivariate normal distribution, A = additive genetic relationship matrix among the animals, I = identity matrix of order equal to the number of observations, $\sigma^2_{a_h}$ = additive genetic variance for trait h, $\sigma_{a_1 a_2}$ = genetic covariance between the traits, $\sigma^2_{e_h}$ = residual variance for trait h, $\sigma_{e_1 e_2}$ = residual covariance between the traits, a_h = breeding values for each animal for trait h, and e_h = error associated to each observation for each trait.

The assumed *a priori* distributions for the parameters of interest were uniform distribution for the systematic effects $\left(\begin{bmatrix} \underset{\sim}{b}_1 & \underset{\sim}{b}_2 \end{bmatrix}\right)$, with normal distributions assumed for the random effects $\left(\begin{bmatrix} \underset{\sim}{a}_1 & \underset{\sim}{a}_2 \end{bmatrix} \mid G\right.$ and $\left.\begin{bmatrix} \underset{\sim}{e}_1 & \underset{\sim}{e}_2 \end{bmatrix} \mid R\right)$. For the covariance matrices G and R for genetic and residual effects, respectively, inverse Wishart distributions were assumed and $G \mid S_a, v_a$ and $R \mid S_e, v_e$, in which S_a and S_e are hyperparameters of the the inverse Wishart distribution for genetic and residual random effects, and v_a and v_e are degrees of freedom of inverse Wishart distribution of genetic and residual random effects, respectively. Information about the *a posteriori* complete conditional distributions is found in Sørensen et al. (2008).

The samples of the complete conditional distributions of covariance components were obtained by Gibbs sampler using the GIBBS1F90 program (Misztal et al., 2015). Chains of 220,000 iterations were considered, with a burn-in of 20,000 iterations and sampling of (co)variance components for each 20 cycles. From each analysis, 10,000 samples were obtained for each trait. The samples of each trait were grouped, totalizing 110,000 samples, and the *a posteriori* means and high posterior density intervals with 90% of samples (HPD90) were estimated. Chain size was defined in preliminary analyses, according to the method of Raftery and Lewis (1992), available in the Bayesian output analysis (BOA) program package (Smith, 2007) of the R software (R Core Team, 2015). The convergence of chains was evaluated by the criterion proposed by Geweke (1992), available in the same package of the same software, and by the visual inspection of the values samples in each iteration.

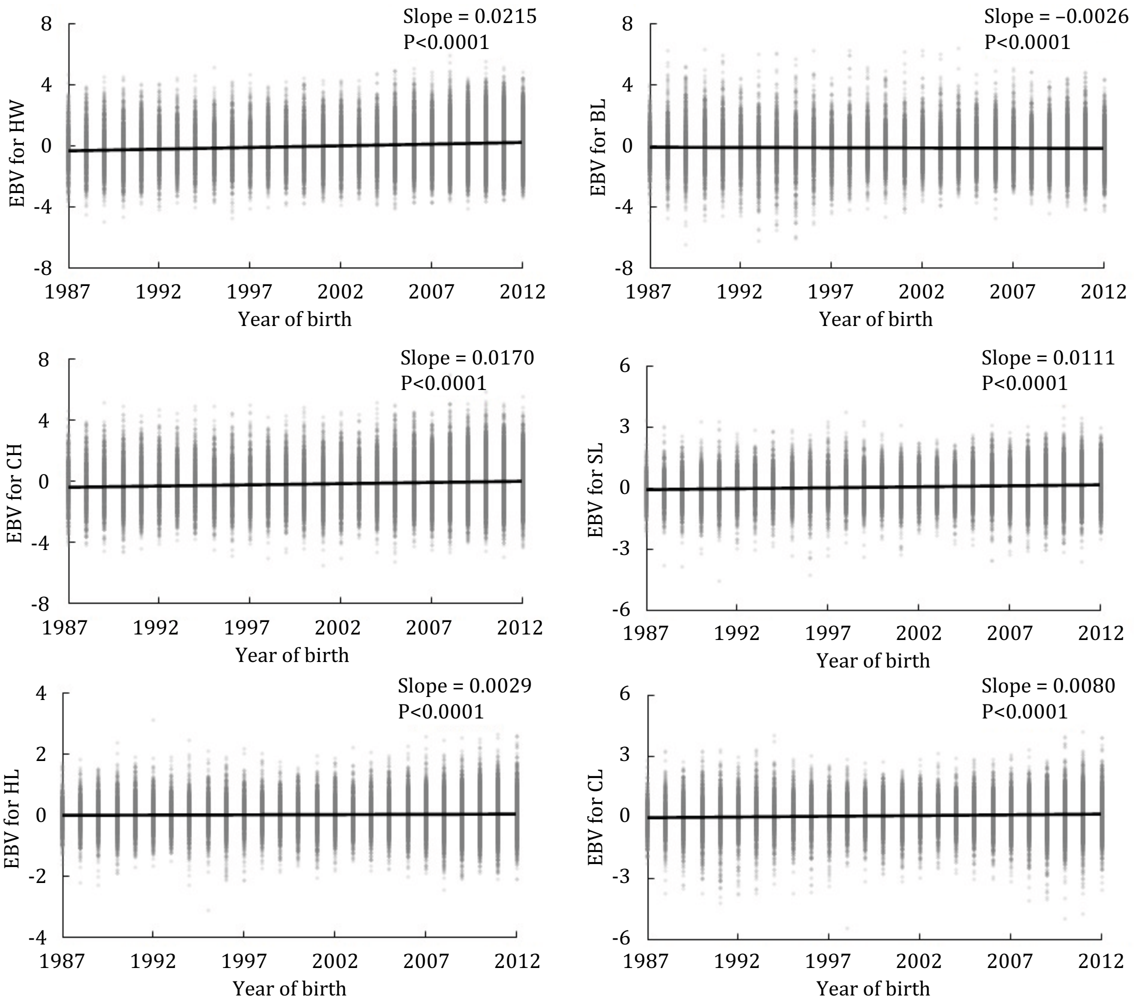
The calculated genetic parameters were heritability (h^2) and additive genetic coefficient of variation (CV_a) using the method developed by Houle (1992), as follows:

$$h^2 = \frac{\sigma_a^2}{\sigma_P^2} \tag{3}$$

$$CV_a\,(\%) = \frac{\sqrt{\sigma_a^2}}{\bar{X}} \times 100 \tag{4}$$

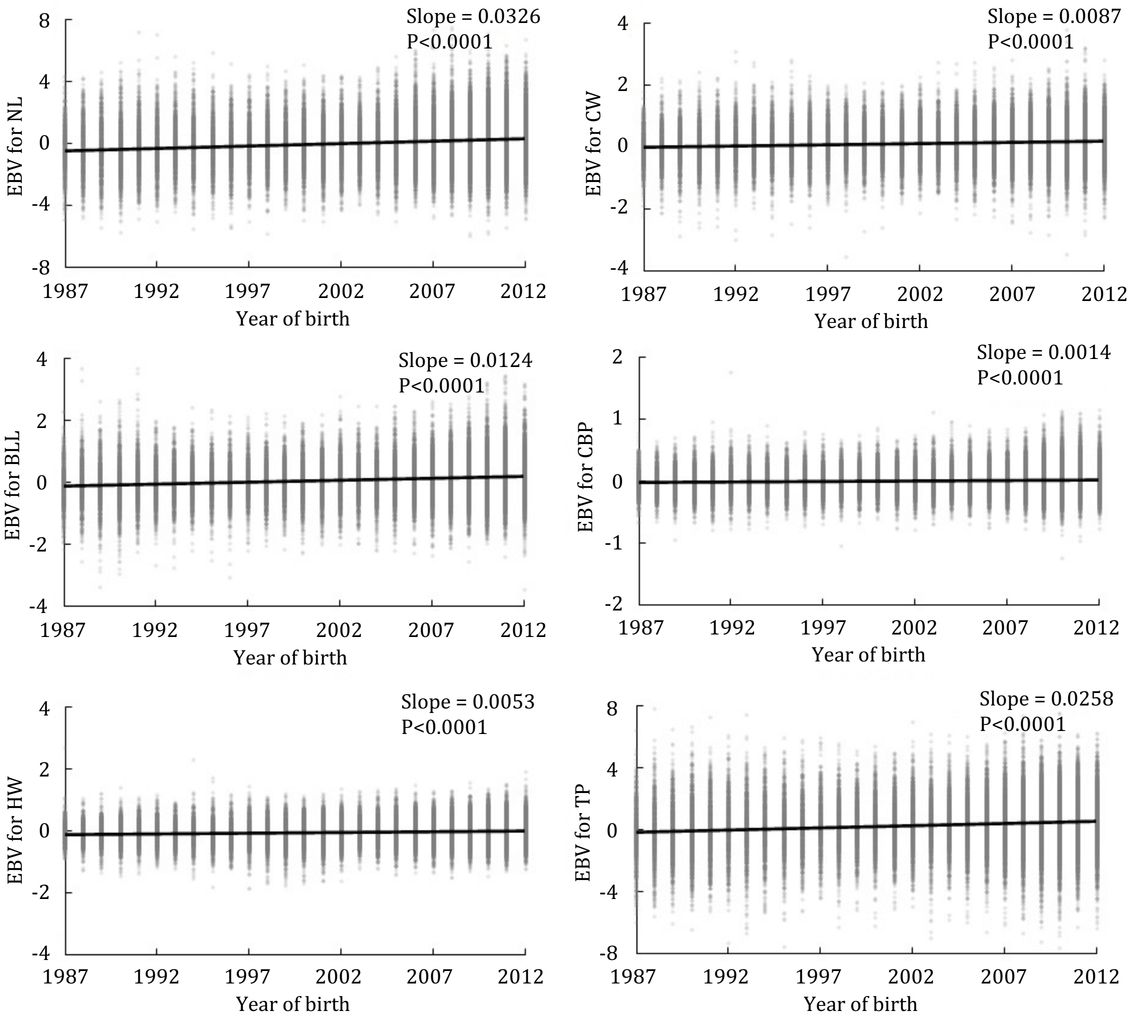
in which $\sigma_P^2 = \sigma_a^2 + \sigma_e^2$ = phenotypic variance for the trait, and $\bar{X}$ = phenotypic mean of the trait.

Genetic trends of the additive genetic effects for each trait were determined as a linear regression coefficient of the estimated breeding values in function of the animal's birth year, and a trend line was generated separately for each trait. As each trait was evaluated 11 times, every animal had 11 different breeding values estimated for the same trait. To perform the linear regression analysis, the estimated breeding values of the animals were considered as the mean of the 11 solutions obtained in the previous analysis. Regression coefficients of the genetic trends were tested by using the F test. To verify the dimension of the angular coefficients of the regression equations, the slopes from Figures 1 and 2 were divided by the phenotypic means of each trait.



The points represent the EBV of each animal, and the line represents the adjusted genetic trends of EBV.

Figure 1 - Regressions of estimated breeding values (EBV) for withers height (WH), croup height (CH), head length (HL), body length (BL), shoulder length (SL), and croup length (CL) in Mangalarga Marchador breed according to the year of birth.



The points represent the EBV of each animal, and the line represents the adjusted genetic trends of EBV.

Figure 2 - Regressions of estimated breeding values (EBV) for neck length (NL), back and loin length (BLL), head width (HW), croup width (CW), cannon bone perimeter (CBP), and thorax perimeter (TP) in Mangalarga Marchador breed according to the year of birth.

3. Results

The estimated heritabilities for all morphometric traits evaluated in Mangalarga Marchador horses ranged from moderate to high magnitude (Table 3), with *a posteriori* means varying from 0.27 for CBP to 0.48 for CH. The additive genetic coefficients of variation (CV_a) were low, with *a posteriori* means varying from 1.23% for BL to 3.82% for NL.

The genetic trends obtained for the 12 studied traits were significant (P<0.0001) in the 26-year period (Figures 1 and 2). Although statistically significant, indicating that there were genetic changes for the traits along the years, the solutions for the slopes were close to 0. For BL, we observed a negative slope, indicating that along the years, there is a trend of reducing BL of Mangalarga Marchador horses (Figure 1).

For the other 11 traits, positive slope values were observed (Figures 1 and 2). The slope values are highly influenced by the scale of the trait, and no comparison can be made about the magnitude of changes between different traits. The percentual changes observed per year for each trait indicates that, for Mangalarga Marchador horses, the traits that changed the most across the years were NL, HW, BLL, and SL, with changes of 0.054, 0.027, 0.026, and 0.022% in the trait per year, respectively.

Table 3 - *A posteriori* means (upper and lower limits of high-density intervals with 90% of samples) of the genetic parameters of morphometric traits of Mangalarga Marchador horses

Trait[1]	σ_a^2 (cm^2)	σ_e^2 (cm^2)	σ_p^2 (cm^2)	h^2	CV_a (%)
WH	4.17 (3.93; 4.43)	4.78 (4.57; 4.94)	8.93 (8.80; 9.06)	0.47 (0.44; 0.49)	1.39 (1.35; 1.44)
CH	4.24 (3.99; 4.49)	4.69 (4.51; 4.87)	8.93 (8.80; 9.06)	0.48 (0.45; 0.50)	1.41 (1.37; 1.46)
HL	0.88 (0.81; 0.95)	2.21 (2.15; 2.27)	3.09 (3.05; 3.13)	0.29 (0.26; 0.31)	1.66 (1.59; 1.73)
BL	3.36 (3.16; 3.55)	5.44 (5.29; 5.59)	8.80 (8.68; 8.91)	0.38 (0.36; 0.40)	1.23 (1.20; 1.27)
SL	1.83 (1.68; 1.98)	4.66 (4.53; 4.79)	6.49 (6.41; 6.58)	0.28 (0.26; 0.30)	2.64 (2.53; 2.75)
CL	1.75 (1.62; 1.88)	3.78 (3.67; 3.88)	5.53 (5.45; 5.60)	0.32 (0.30; 0.34)	2.62 (2.52; 2.71)
NL	5.41 (5.05; 5.75)	8.04 (7.77; 8.30)	13.45 (13.26; 13.64)	0.40 (0.38; 0.43)	3.82 (3.70; 3.95)
BLL	1.23 (1.12; 1.32)	3.03 (2.94; 3.11)	4.25 (4.19; 4.31)	0.29 (0.27; 0.31)	2.28 (2.19; 2.37)
HW	0.33 (0.31; 0.35)	0.60 (0.58; 0.62)	0.93 (0.91; 0.94)	0.35 (0.33; 0.37)	2.87 (2.79; 2.96)
CW	1.07 (0.99; 1.15)	2.53 (2.46; 2.60)	3.60 (3.55; 3.65)	0.30 (0.28; 0.32)	2.09 (2.01; 2.17)
CBP	0.14 (0.13; 0.15)	0.36 (0.35; 0.37)	0.50 (0.49; 0.51)	0.27 (0.25; 0.29)	2.06 (1.98; 2.16)
TP	8.06 (7.44; 8.70)	18.32 (17.79; 18.81)	26.38 (26.03; 26.74)	0.31 (0.28; 0.33)	1.66 (1.60; 1.72)

σ_a^2 - additive genetic variance; σ_e^2 - residual variance; σ_p^2 - phenotypic variance, h^2 - heritability, CV_a - additive genetic coefficient of variation.

[1] Abbreviations and definitions of traits, see Table 1.

4. Discussion

The phenotypic means observed for WH (Table 2) are within the range (140.0 to 157.0 cm) required by the ABCCMM for the horse's registration (ABCCMM, 2020). The other measures have no restrictions on measures described in the racial pattern.

The moderate to high heritability values verified by the present work (Table 3) indicate that it is possible to achieve genetic gains for the studied traits throughout selection, indicating that these traits can be used as selection criteria in Mangalarga Marchador breeding programs. For WH, heritabilities of 0.21 for Spanish Purebred (Sánchez et al., 2013), 0.27 for Murgese (Bramante et al., 2016), and 0.43 for multiple breed analysis of Quarter Horse, Arabian, and Mangalarga, (Faria et al., 2004) were estimated.

For some of the length-related traits (HL, BL, SL, CL, NL, BLL), the heritabilities were already estimated for other breeds. Head length of Spanish purebred horses is a trait with moderate heritability (0.35; Sánchez et al., 2013), similar to the magnitude observed in Mangalarga Marchador horses (0.29; Table 3). Low heritability was estimated for CL (0.15) by Sánchez-Guerrero et al. (2017) for Spanish Purebred horses, while for Mangalarga Marchador horses, this trait is of moderate heritability (0.32; Table 3). Lastly, for NL, low to high heritabilities were estimated for both Spanish purebred (0.14; Sánchez et al., 2013) and Mangalarga Marchador (0.40; Table 3) horses.

The HW was the only width-related trait that we studied that was already evaluated for other breeds. Heritabilities of 0.15 (Sánchez-Guerrero et al., 2017) and 0.09 (Sánchez et al., 2013) were estimated for this trait in Spanish purebred animals. These values are lower than the heritability for HW in Mangalarga Marchador horses that was of moderate magnitude (0.35). The last measures we studied were the perimeter-related ones, CBP and TP. These traits were evaluated by Faria et al. (2004) in Quarter horses and Arab and Mangalarga foals, and their heritabilities were of moderate and high magnitude (0.54 for TP and 0.38 for CBP). For Spanish purebred horses, heritability estimates of CBP ranged from 0.30 to

0.53 (Molina et al., 1999; Sánchez et al., 2013; Sánchez-Guerrero et al., 2017). Molina et al. (1999) also estimated heritability of 0.48 for TP in Spanish purebred. For Murgese horses, the heritabilities of CBP and TP were 0.31 and 0.24, respectively (Bramante et al., 2016). In general, what can be observed for CBP and TP is that they are moderate to highly heritable traits in multiple breeds of horses, including Mangalarga Marchador (heritabilities of 0.27 and 0.31 for CBP and TP, respectively; Table 3).

The results of the studies cited are different from those presented herein not only for analyzing data from different breeds but also for using different methodologies in the measurement of the traits used to estimate the genetic parameters. In the present study, the morphometric measurements were taken directly on the body of the animals using metric instruments, while the other authors (Sánchez et al., 2013; Sánchez-Guerrero et al., 2017) used a linear scoring system for visual evaluation to assign values to different body regions. According to Sánchez et al. (2013), genetic parameters obtained through the linear scoring system are also able to generate quality information for conformation traits for the Spanish Purebred. However, the measurement can be more reliable than the scoring system used in some breeds, since it is obtained directly on the animals, in contrast to the score that is done subjectively and in some cases by more than one evaluator.

The low values found in the present study for the additive genetic coefficients of variation (CV_a) demonstrate that the 12 morphometric traits present low evolutionary potential, even with high values for heritabilities. These contradiction between CV_a and heritabilities highlight the importance of carrying out a joint evaluation of these parameters (Hansen et al., 2003). High heritability values only suggest that genetic variability explains a high proportion of phenotypic variability and does not indicate the magnitude of this variability (Hansen et al., 2003). When we calculate CV_a, which is standardized by the mean of the trait instead of the variance, we can analyze the magnitude of the genetic variances in a more direct way. In fact, we believe that we have low genetic variability for the traits because of the low phenotypic variability of the dataset (Table 2). A possible reason for this low variability is the fact that only animals that follow a very strict pattern can be registered as purebred. However, we know that animals known to be purebred (offspring of parents with definitive register) can be outside the patterns and when this happens, the measures of these animals are not registered by the breeders association technicians. These exclusions indicate that possibly we are not capable to capture the real phenotypic variance of the traits on field, and consequently we also can not capture the genetic variability. Most important, this reduction in the variance we can capture is compromising our capability of estimating the evolutional potential of Mangalarga Marchador population for each trait.

At this point, it should be highlighted that for the Mangalarga Marchador breed, it is not expected to practice selection aiming to change the morphological types – since they are pre-established as breed standards; therefore, little change in the size of the animals is desirable. However, there is evidence of association between gait and morphometry, and for the traits related to gait, we expect to achieve improvements in the animals throughout selection. Besides the association between gait and morphometry, which was not analyzed in the present study, it is important to evaluate the evolutive potential of morphometry traits to know to which extend genetic selection can modify these traits. Regardless of the interest in the direction of selection, knowledge of genetic trends is critical to the description of the effect of selection process over time.

The slopes obtained for EBV regressions according to the birth year of horses were in general positive (except BL) and always significant, indicating that the animals tended to get shorter in length over the years, but bigger in the other evaluated dimensions (Figures 1 and 2). For Mangalarga Marchador horses, it is not possible to evaluate if these changes happened in a favorable sense, since there is no agreement about which is the favorable sense of change that is expected for each trait. Furthermore, the changes observed per year were small, so considerable changes in the breed standard will not be observed in a long time. The results presented here indicate that, at some point, if the direction of selection does not change, the limits determined for WH to register the animals will have to change, otherwise, more horses will be declassified each year.

Contrarily to Mangalarga Marchador horses, for other breeds, the direction of selection is more well defined for each trait. Costa et al. (2001) evaluated the genetic trends of 10 morphometric measures (WH, CH, HL, BL, CL, NL, BLL, HW, CW, and breast width) of Brazilian pony breed, and found negative values for all measurements during the evaluated period. These authors found that these results were favorable for almost all measures, except for BLL, CW, and breast width, once it is desirable to reduce measures in the breed, as the smaller animals are more valued. These results are a good example of how the ideal direction of selection changes from breed to breed; furthermore, and more important, they show that the phenotypic means of morphometric traits of horses might be increased or decreased by selection, depending on the interest.

5. Conclusions

The heritabilities for morphometric traits of Mangalarga Marchador horses are from moderate to high, indicating that these traits can be changed by genetic selection.

The low phenotypic variability represents an obstacle to infer about the evolutionary potential of Mangalarga Marchador horses. Including information from purebred animals that do not match the breed standard in the breeders association database could help capture the real variability of traits.

The morphometry of Mangalarga Marchador horses significantly changed in the past years, although no directional selection has been practiced, neither the breed has an official breeding program designed in Brazil.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Data curation: S. Maruch, G.C. Gouveia and F.L.B. Toral. Formal analysis: S. Maruch, G.C. Gouveia, V.M.P. Ribeiro, L.R.A. Abreu and F.L.B. Toral. Investigation: S. Maruch. Methodology: G.C. Gouveia and F.L.B. Toral. Resources: S. Maruch. Validation: S. Maruch. Visualization: A.S.C. Rezende, V.M.P. Ribeiro and L.R.A. Abreu. Writing-review & editing: S. Maruch, G.C. Gouveia and F.L.B. Toral.

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